Probe

Newsletter for the USDA Plant Genome Research Program

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Benefits of U.S. Agricultural Research

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Department of Agricultural Economics
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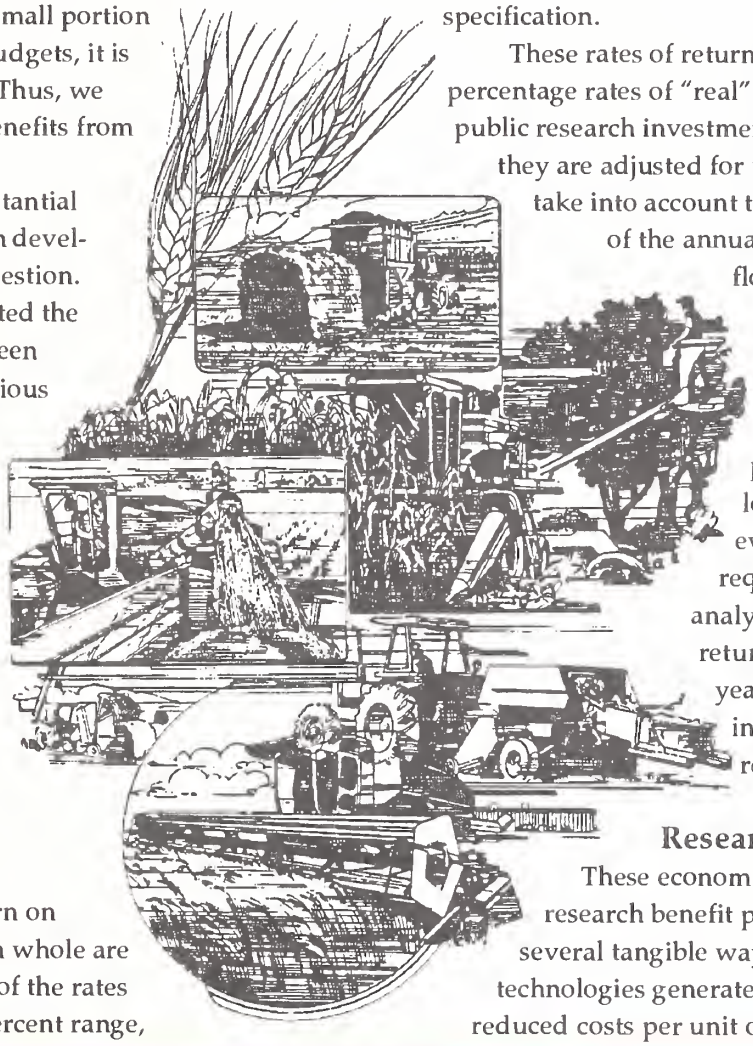
Public expenditures on agricultural research in the United States currently exceed $2.5 billion annually. Although this amount is a small portion of total Federal and State budgets, it is still a great deal of money. Thus, we ought to ask how society benefits from this investment.

Since the 1950s, a substantial body of knowledge has been developed to help answer this question. Several studies have estimated the statistical relationship between agricultural output and various inputs, including agricultural research. The results of these analyses have been used to calculate economic rates of return on research investment. This type of calculation has been completed for agricultural research as a whole and for research on individual commodities.



Rates of Return

The estimated rates of return on research for agriculture as a whole are presented in Table 1. Most of the rates of return are in the 30-60 percent range, several times the return typically obtained from conventional investments in manufacturing. These returns do not mean that all agricultural research is worthwhile. Some projects or programs have very high (several hundred percent) rates of return while others have low or no return. Also, the variation in rates of return shown in Table 1 reflect differences in time periods and model specification.

These rates of return measure the annual percentage rates of "real" returns on the previous public research investments -- "real" meaning that they are adjusted for inflation. The calculations take into account the estimated time pattern of the annual benefits and convert the flow of benefits to an annualized basis. This time pattern arises because research knowledge may take several years to produce, then pay off for a long period of time, and eventually depreciate and require maintenance. A recent analysis found roughly a $5 return, spread over a 15- to 20-year period, for each dollar invested in agricultural research.

Research Benefits

These economic returns on investment in research benefit producers and consumers in several tangible ways. First, adoption of new technologies generated by research leads to reduced costs per unit of production and ex-

panded supplies of food and fiber. Expanded supplies put downward pressure on prices, thus benefiting the consumer. This benefit is particularly important for low-income consumers who spend a higher proportion of their budget on food than do high-income consumers.

Second, improvements in agricultural productivity have enabled farmers to remain competitive in world markets and to expand exports. Third, agricultural advances have a multiplier effect on the rest of the economy by generating jobs and incomes in the nonfarm sector. This in turn expands tax revenues, thus offsetting the initial public expenditures on research.

Fourth, agricultural research has led to improvements in food quality, food safety, and nutrition. Researchers have developed more nutritious foods with less waste. Food processing, packaging, and preparation research has led to reduced spoilage and contamination. Fifth, agricultural research has contributed technical and institutional solutions to improve environmental quality. For example, minimum tillage farming systems conserve energy and reduce erosion; integrated pest management research is showing the way to less pesticide-intensive farming.

Education and Productivity

Sixth, the complementary relationship among research, teaching, and extension programs in our universities means that students, farmers, government officials, and agribusiness leaders have received more sophisticated up-to-date training than if our university teachers and extension workers just passed on the knowledge they were taught.

Seventh, agricultural research has eased the drudgery and extended the productive worklife of the farmer. Machines, equipment, and chemicals now perform tasks formerly completed in a backbreaking manner. Eighth, agricultural research has generated information that can be used to improve government policies or other institutional arrangements that affect the well-being of producers and consumers.

Table 1. Estimated Rates of Agricultural Research for the United States.

Study	Time Period	Annual Rate of Return (%)
Griliches, 1964	1949-1959	35-45+
Lattimer, 1964	1949-1959	not significant
Evenson, 1968	1949-1959	47
Cline, 1975	1949-1958	39-47+
	1954-1968	32-39+
	1967-1972	28-35+
Peterson & Fitzharris, 1977	1957-1962	49+
	1967-1972	34+
Evenson, Waggoner, & Ruttan, 1979	1948-1971	45+
Davis, 1979	1949-1959	
	1964-1974	
White, Havlicek, & Otto, 1979	1942-1957	48
	1958-1977	42
Lyu, White, Liu, 1984	1949-1981	66
Braha & Tweeten, 1986	1959-1982	47
Huffman & Evenson, 1989	1950-1982	43
Norton & Ortiz, 1992	1987	30

+ Return to research and extension combined.

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Conclusion

In conclusion, the United States has made a sizable investment in its agricultural research system. This investment has paid handsome dividends to producers and consumers. Estimated real rates of return of 30-60 percent are not uncommon. And these returns only represent part of the benefits. Food safety and environmental improvement benefits of research have increased in recent years as these factors command more of a central focus in research programs.

References

Braha, H., and L. Tweeten. "Evaluating Past and Prospective Future Payoffs from Public Investment to Increase Agricultural Productivity." Technical Bulletin T-163, Agricultural Experiment Station, Oklahoma State University, September 1986.

Cline, L. "Sources of Productivity Change in United States Agriculture." Ph.D. dissertation, Oklahoma State University, 1979.

Davis, S. "Stability of the Research Production Coefficient for U.S. Agriculture." Ph.D. dissertation, University of Minnesota, 1979.

Evenson, R. "The Contribution of Agricultural Research and Extension to Agricultural Production." Ph.D. dissertation, University of Chicago, 1968.

Evenson, R.E., P.E. Waggoner, and V.W. Ruttan. "Economic Benefits from Research: An Example from Agriculture." *Science* 205(September 14, 1979):1101-1107.

Griliches, Z. "Research Expenditures, Education, and the Aggregate Agricultural Production Function." *American Economics Review* 54(December 1964):961-974.

Huffman, W.E. and R.E. Evenson. "The Development of U.S. Agricultural Research and Education: An Economic Perspective, Part V," Staff Paper No. 175, Economics Department, Iowa State University, December 1989.

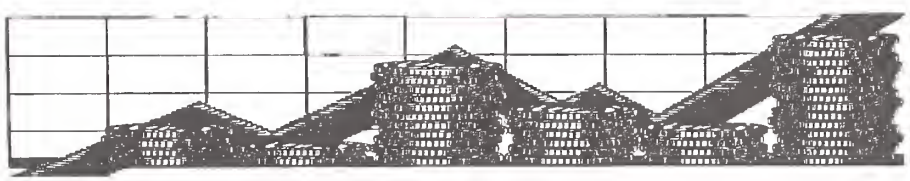
Lattimer, R. "Some Economic Aspects of Agricultural Research and Extension in the U.S." Ph.D. dissertation, Purdue University, 1964.

Lyu, S.L., F.C. White, and Y.C. Liu. "Estimating the Effects of Agricultural Research and Extension Expenditures on Productivity: A Translog Production Function Approach." *Southern Journal of Agricultural Economics* 16(December 1984):1-8.

Peterson, W.L. and J.C. Fitzharris. "The Organization and Productivity of the Federal State Research System in the United States," in *Resource Allocation and Productivity in National and International Research*, Thomas M. Arndt, Dana G. Dalrymple, and Vernon W. Ruttan, eds., Minneapolis: University of Minnesota Press, 1977, pp. 60-85.

White, F., J. Havlicek, Jr., and D. Otto. "Fifty Years of Technical Change in American Agriculture." Paper presented at the International Conference of Agricultural Economists, Banff, Canada, September 3-12, 1979.

Norton, G.W. and J. Ortiz. "Reaping the Returns to Research," *Journal of Production Agriculture*, March-April 1992 (in press). ◆



Arabidopsis Database Now Available

A specialized genome database on the small plant *Arabidopsis thaliana* is now available to assist research scientists.

Dr. Howard Goodman and associates developed the database at the Massachusetts General Hospital with funds from the USDA Plant Genome Research Program through the National Agricultural Library (NAL). Eventually An *Arabidopsis thaliana* Database, known as AAtDB, will be integrated into NAL's Plant Genome Database.

AAtDB is available for public distribution. The database runs on a stand-alone Sun Microsystem work station as an X-windows application. Within the next 6 months, an Apple Macintosh version will be available. AAtDB is being distributed via Internet anonymous file transfer protocol (FTP) procedure.

For more information, contact Dr. Sam Cartinhour or Dr. J. Michael Cherry via Internet computer mail at "curator@frodo.mgh.harvard.edu" or via FAX (617) 726-6893. (Also see the *Arabidopsis* database article in the Spring '92 issue of *Probe*.)

Taking Stock

Arabidopsis Stock Center--Open for Business

Dr. Randy Scholl, Research Geneticist
Department of Molecular Genetics, Ohio State University
Columbus, OH

Orders for seeds and DNA are now being filled at the *Arabidopsis* Biological Resource Center at Ohio State University.

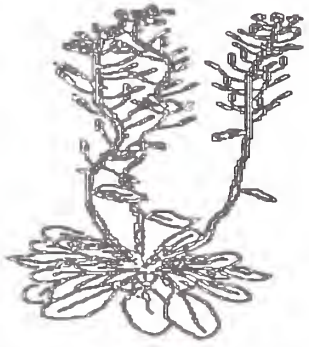
Five general classes of stocks are available from the Center, as described in the April 1992 Seed and DNA Stock List. Included are (1) mutants, (2) marker lines for genetic mapping, (3) ecotypes, (4) RFLP bacteriophage clones, and (5) RFLP cosmid clones. All are available for immediate shipment.

The Center's current seed stocks should be useful to the *Arabidopsis* and plant research community. The following examples demonstrate their usefulness:

1) Mutants induced by T-DNA seed transformation, provided by Dr. Kenneth Feldmann of the University of Arizona, are potentially molecularly tagged for a variety of types of genes. The Center currently possesses transformed lines having late flowering, floral morphology, and reduced fertility phenotypes. Other classes of T-DNA induced visible mutants will be received soon.

2) Mutants of many types induced by chemical mutagenesis and radiation, as well as stocks developed for study of linkage on each of the five *Arabidopsis* chromosomes, are available. These stocks were provided by the Nottingham *Arabidopsis* Stock Center; the markers were developed by Dr. Maarten Koornneef and coworkers.

3) A set of recombinant inbred (RI) lines were developed at DuPont



Co. by Drs. Robert Reiter and Pablo Scolnik and coworkers. They are expected to be widely used for mapping of DNA markers including RFLPs and RAPDs.

DNA Stocks

The DNA stocks presently available for distribution are collections of clones identifying polymorphisms. These stocks include 70 bacteriophage clones from Dr. Elliot Meyerowitz and colleagues of the California Institute of Technology, and approximately the same number of cosmid clones from Dr. Howard Goodman and coworkers of the Massachusetts General Hospital. More RFLP-associated clones are currently being received.

Included among DNA stocks that will be available in the near future are clone libraries. A set of yeast artificial chromosome (YAC) libraries, developed by Drs. Chris Somerville and Erwin Grill at Michigan State University, became available for distribution in June 1992. The YAC library of Dr. Eric Ward of Ciba/Geigy Corp. became available in July 1992.

At present, the above stocks are being provided to researchers free of charge. Orders are accepted by mail, electronic mail, facsimile, or telephone as follows:

MAIL: The *Arabidopsis* Biological Resource Center at Ohio State University, 1735 Neil Avenue Columbus, OH 43210, USA

E-MAIL, Information: arabidopsis+@osu.edu

E-MAIL, Seed Orders: seeds@genesys.cps.msu.edu (Type "stockorder" on the subject line.)

E-MAIL, DNA Orders: dna@genesys.cps.msu.edu (Type "stockorder" on the subject line.)

FAX: 614-292-0603

TELEPHONE: 614-292-9371

TELEPHONE, Seed Inquiries: 614-292-1982 (Randy Scholl)

TELEPHONE, DNA Inquiries: 614-292-2115 (Keith Davis)

The seed and DNA stock list can be obtained by notifying the Center through one of the above means. You may also have your name added to the mailing list.

Future Plans

For the near future, several types of new stocks will be obtained. Included will be pooled populations of T-DNA transformants from Dr. Feldmann, which should be available by June 1992.

Dr. Sakti Pramanik and colleagues at Michigan State University are working to develop an *Arabidopsis* database, known as the *Arabidopsis* Information Management System (AIMS). A prototype version of the system should be running shortly so that stocks can be ordered directly through the computer system. This will allow for immediate updates of available stocks as they are added to the list, and will prove especially valuable during this developmental phase when new stocks are added rapidly to the collection.

The Center is funded by a grant from the National Science Foundation. Those of us with the Center are pleased to be able to serve the plant community. If you have any questions, do not hesitate to contact Randy Scholl (Center director and head of the seed laboratory) or Keith Davis (associate director and head of the DNA laboratory). ◆

Touching Base with Olin Anderson

Wheat Database Project-Coordinators, Goals, and Accomplishments

Olin Anderson, Research Geneticist
USDA, Agricultural Research Service
Western Regional Research Center
Albany, CA

Efforts are underway to assemble a wheat prototype database, a goal of the U.S. Department of Agriculture's (USDA) Plant Genome Program. The database will be maintained at the Agricultural Research Service's (ARS) Western Regional Research Center in Albany, CA. Coordinator for the project is ARS Researcher Olin Anderson.

The primary goals of the project are to establish the hardware and software systems to construct and maintain a wheat database and to coordinate the loading of all available and useful data. The initial priority is to accumulate genome mapping and probe/clone/library information. Additional data areas will include information on wheat germplasm, including pedigrees, and data on wheat genetics and traits.

Design and Implementation

The wheat database prototype is being designed and implemented in cooperation with the Computer Science Division of the Lawrence Berkeley Laboratory. John McCarthy (Phone: 510-486-5307) is the principal contact. The prototype will operate on a Sun workstation at Albany (plus mass storage devices) operating as a server. Access will initially be limited to designated users who are able to connect to INTERNET. The updated database will periodically be copied to the master plant database being organized at USDA's National Agricultural Library. The master database is intended as the resource for general public access.

The Albany site will also provide molecular biological support to mapping and map utilization. Persons involved in the project are establishing a repository of probes and clone libraries of the Triticeae, with initial emphasis on wheat. The repository, to be supervised by Susan Altenbach, will serve as both permanent storage and at least initial distribution of probes and libraries. Plans are to exchange probes and duplicate the repository at other sites world wide. Also to be explored is

the development of additional molecular biological resources for Triticeae research; that is, the construction and utilization of improved and novel recombinant libraries, and mapping technology support.

Data Coordinators

Participants in the project have identified some specific areas that require data assembly and organization, and, as a result, have selected subject-area coordinators. Many areas are overlapping and will require input from several areas of expertise. As the need becomes apparent, "subcommittees" will form around broad topics. The following is a list of the coordinators and subject areas:

Cytology:

Bikram Gill, Department of Plant Pathology, Kansas State University, Throckmorton Hall, Manhattan, KS 66506 Tel: 913-532-6176, FAX: 913-532-5692

Database Assembly, and Maintenance:

Olin Anderson, USDA, ARS, WRRC, 800 Buchanan Street, Albany, CA 94710 Tel: 510-559-5773, FAX: 510-559-5777

Genetics, Nomenclature:

Gary Hart, Department of Soil & Crop Sciences, Texas A&M University, College Station, TX 77843 Tel: 409-845-8293, FAX: 409-845-0456

Genetic Stocks:

Perry Gustafson, USDA, ARS, Department of Agronomy, University of Missouri, Columbia, MO 65211 Tel: 314-882-7318, FAX: 314-875-5359

Germplasm:

Ken Kephart, 214 Waters Hall, University of Missouri, Columbia, MO 65211 Tel: 314-882-2001, FAX: 314-884-4317

Pathology:

David Porter, USDA, ARS, Oklahoma State University, Stillwater, OK 74075 Tel: 405-624-4212, FAX: 405-372-1398

Probe/Library Repository:

Susan Altenbach, USDA, ARS, WRRC, 800 Buchanan St., Albany, CA 94710 "altenbach @ sun-dq.pw.usda.gov" Tel: 510-559-5716, FAX: 510-559-5777

Proteins, Gel Patterns, Wheat Quality:

Bob Graybosch, USDA, ARS, Department of Agronomy, 322 Keim Hall, University of Nebraska, Lincoln, NE Tel: 402-472-1563, FAX: 402-437-5234

Triticeae Mapping Initiative

To facilitate the gathering of mapping data, the database personnel are working closely with the International Triticeae Mapping Initiative (ITMI) organization. ITMI is an international group with the purpose of facilitating the mapping and dissemination of resulting data of important members of the grass tribe Triticeae, which includes wheat, rye, barley, ancestral species, and related wild grasses. Dr. Calvin Qualset (Chairman, Department of Agronomy & Range Science, University of California, Davis) is ITMI coordinator. (See *Probe* Spring 1992)

Mapping Coordinators

Wheat, rye, and barley, along with many wild relatives, are syntenic--they possess homologous linkage groups with similar linear arrangements of the same genes. To facilitate the collation of data produced by different laboratories in different countries, seven members of ITMI have agreed to serve as coordinators for the seven linkage groups.

Group 1:

Rudi Appels, CSIRO, GPO Box 1600, Canberra, Australia 2601 Tel: 61 62 464496, FAX: 61 62 465000

Group 2:

Peter Sharp, Plant Breeding Institute Cobbitty Road, Cobbitty, NSW 2570, Australia Tel: 61 46 512600, FAX: 61 46 512578

Group 3:

Mark Sorrells, Department of Plant Breeding and Biometry, Cornell University, Ithaca, New York 14853 Tel: 607-255-1665, FAX: 607-255-6683

David Hoisington, Molecular Biology Lab, CIMMYT, Lisboa 27, Colonia Juarez, Apdo, Postal 6641 06600 Mexico DF, Mexico Tel: 52 5 761 3311 FAX: 52 5 954 1069

Group 4:

Jan Dvorak, Department of Agronomy & Range Science, University of California-Davis, California 95616 Tel: 916-752-6549 FAX: 916-752-4361

Group 5:

Bikram Gill (address previously listed)

Group 6:

Gary Hart (address previously listed)

Group 7:

Michael Gale, Cambridge Laboratory, Colney Lane, Norwich, Norfolk NR4 7UJ, United Kingdom Tel: 44 603 52571 FAX: 44 603 502270

Rye and Barley

Rye is a critical part of wheat breeding programs because of the importance of rye genes that are desirable to cross into wheat. Perry Gustafson, ARS, University of Missouri, is coordinating the rye genome map. Similarly, information on barley is of critical interest to wheat researchers. The input of barley data is being coordinated by Andris Kleinhofs at Washington State University.

Barley:

Andris Kleinhofs, Department of Crop and Soil Sciences, Washington State University, Pullman, WA 99164 Tel: 509-335-4389 FAX: 509-335-3475

Rye:

Perry Gustafson (address previously listed)

Ancestral Genomes

Since the wild ancestral genomes of wheat and wild grasses amenable to breeding into wheat are critical sources of potential new genes for traits such as yield and pest and stress resistance, the databases will also contain results of mapping programs from these genomes as the data becomes available. Currently two of the ancestral genomes are being actively mapped:

A-genome

Rudi Appels & Mark Sorrells

D-genome

Bikram Gill & Rudi Appels

Cooperative Agreements

Contracts are in force or are now being arranged for data assembly and input into the databases. A contract to ITMI (Cal Qualset) is assisting in mapping coordination by ITMI and resource development with Jan Dvorak (UC Davis) and Gary Hart (Texas A&M). Mark Sorrells and Steven Tanksley (Cornell) have support for a programmer position for data input and for the development of software routines, along with the necessary hardware to serve as a major site of data input. Cornell will also assist the Barley Mapping Group in data input. Bikram Gill (Kansas State) will be overseeing the assembly of wheat cytogenetic data for the database. Wheat nomenclature and genetics will be contributed by Gary Hart (Texas A&M).

Data on North American wheat cultivars was already being cataloged by Ken Kephart (Missouri). He will coordinate germplasm information with other databases such as the Germplasm Resources Information Network (GRIN) with the USDA Small Grains Repository at Aberdeen, ID, and CIMMYT in Mexico City. Also at Missouri is Perry Gustafson who will coordinate and input data on genetic stocks. Future cooperative agreements may be arranged for other areas such as pathology and wheat storage proteins. David Porter (Oklahoma State) is assembling examples of data on pathology and pests to assess for database design and input. Grain proteins are a major contributor to quality traits in wheat. Examples are being organized by Bob Graybosch at Nebraska. ◆

Home Base

Plant Genome Database To Release Data in ASN.1 Format

Douglas Bigwood, Database Manager
Plant Genome Data and Information Center
National Agricultural Library, USDA
Beltsville, MD

One of the difficulties in making use of data from a database is in interpreting the format of the data. A common approach in the past has been to release data in a so-called flat file format. However, this format fails to preserve the inherent relationships in a more complex data model--for example, a relational database management system such as the Sybase software used for the Plant Genome Database.

A better approach is to make the data available according to a specification defined in a data description language. Abstract Syntax Notation 1 (ASN.1) is one type of data description language. Data from the Plant Genome Database is to be made available in the ASN.1 format in addition to its primary means of access, which will be on-line. Also, data exchange between NAL and our collaborators will most likely occur using ASN.1. The article by Jim Ostell of the National Library of Medicine's National Center for Biotechnology Information describes ASN.1 and some advantages in its use. ◆

Touching Base with John Imsande

"Soybase"(Soybean Genome Database) Incorporates Biochemical Pathways

John Imsande, Professor
Department of Agronomy
Iowa State University
Ames, IA

Soybean production contributes approximately $10 billion annually to the U.S. economy. Currently, the most desirable attributes of the soybean seed are its high contents of protein and oil. A better understanding of the genetics of soybean may allow not only for increased seed production but also for increased protein content and a more desirable oil content.

Biochemical Pathways

The genetics of an organism is reflected in its physiology. As complex as physiological traits are, they can be broken down into discrete biochemical pathways and discrete biochemical reactions. Drs. John Imsande, Iowa State University, and Tom Cheesbrough, South Dakota State University, are working with USDA's Plant Genome Office to develop a prototype database of plant biochemical pathways.

Part of "Soybase"

Imsande is developing a database for nitrogen uptake, assimilation, metabolism, and utilization; Cheesbrough is developing a database for lipid metabolism. Upon completion, the biochemical pathways database will become part of "Soybase," the prototype genome database being developed for soybean.

> *Soybean production contributes approximately $10 billion annually to the U.S. economy.*

The scientists are compiling data on enzymes, reactions, reactants, products, optimal physiological conditions, genetic regulation, physical properties, genotypic source, availability of mutants in pathways, and many other types of information. Working together, they are developing a structural design for entering data that will be adaptable to almost any biochemical pathway.

Data Review

Once the prototype data structure is assembled and data have been collected from the literature and entered into the database, Imsande and Cheesbrough will contact experts in each topic area to review the data for accuracy and completeness.

For further information concerning the design and development of the plant biochemical pathways database, please contact:

Dr. John Imsande
Dept. of Agronomy
Iowa State University
(515) 294-2505

Dr. Tom Cheesbrough
Biology/Microbiology Dept.
South Dakota State University
(605) 688-5504 ◆

Jen Leaves NRICGP

Dr. George Jen, NRICGP Program Director for the 1992 Plant Genome Program, departed the office on June 30 to pursue a law career. He will attend Georgetown Law School and work as a law clerk in a local firm that specializes in intellectual property rights.

The National Research Initiative Competitive Grants Program soon will be seeking a plant geneticist for the position of Plant Genome Program Director.

Touching Base with Mary Berlyn

Maize Database Implementation--Unveiling at Annual Meeting

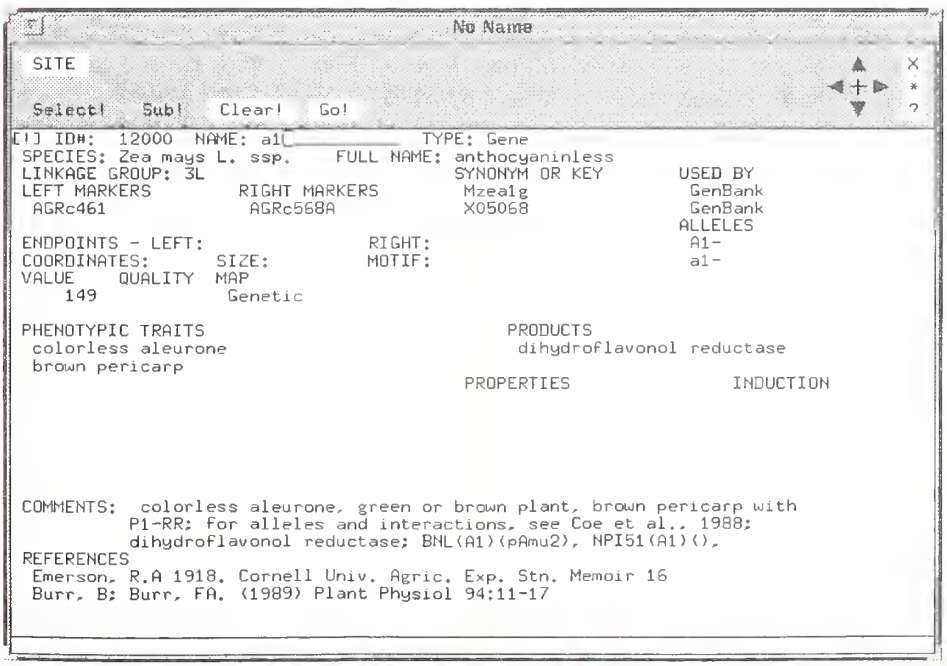
Mary Berlyn, Research Scientist, Department of Biology and School of Forestry and Environmental Studies, Yale University, and Stan Letovsky, President, Letovsky Associates, New Haven, CT

Maize geneticists had an opportunity to use the Sun SparcStation Sybase implementation of the Maize DB (Database) at their annual maize genetics meeting in Asilomar, CA, last March.

The scientists queried for stocks with specific genotypic combinations, map diagrams of gene and RFLP marker positions or cytogenetic markers, phenotypic traits associated with specific mutations, genes producing specific gene products or product classes, and the converse of such queries.

Interest in the database was high. Scientists from both academia and industry expressed satisfaction and support for the project, which is headed by USDA Agricultural Research Service Geneticist Ed Coe at the University of Missouri.

The demonstration allowed participants to query with the entire suite of first-phase, fully functioning software, with comprehensive data entry in many areas--including Maize Genetics Cooperation Stock Center and other stocks, genes, gene products, and mutations--and with more limited entries of mapping data.



Database Development

The demonstration culminated a year of work that began, symmetrically enough, with the first meeting of the Maize Database Advisory Group recruited and convened by Ed Coe at the 1991 Annual MAIZE GENETICS Meeting in Delavan, WI. This group subsequently met to recommend priorities and requirements, and provide general advice for the development of the database.

A University of Missouri working group--Ed, Denis Hancock, Mary Polacco, and Marty Sachs--periodically met with Mary Berlyn, Yale University, and Stan Letovsky, Letovsky Associates, to further develop design specifications. After further work on the design, completed by Stan and Mary in September, the specifications were converted into database software by Stan. The Maize DB implementation in Sybase was delivered to the Columbia, MO, group in November 1991. Heavy-duty data entry work in Columbia and New Haven, and small modifications in the software followed.

At the March maize genetics meeting, Denis and Stan installed the database on a workstation in the poster hall (and an on-line vt100 version ran on a portable computer connected to the server in Columbia). The database developers then all vied to show their favorite features of Maize DB to interested participants.

Contents

Some of the contents and relationships within the database are indicated in the following statements. (Capitalized nouns indicate major objects in the database.)

- The genome of an individual or species is made up of chromosomes and chromosome arms, described as LINKAGE GROUPS.
- Intervals on Linkage Groups are described as SITES. Types of Sites include genes, RFLP-defined regions, sequenced regions, knobs, centromeres, and translocation breakpoints.
- MUTATIONS are changes of Sites, for example, an allele of a gene; an inversion of a chromosomal segment; restriction fragment polymorphisms within a probed site; or a reciprocal exchange at two breakpoints.
- SITES have coordinates or endpoints; a map is dynamically generated by ordering these values along a coordinate axis. A site can have different coordinate values assigned to it in different map coordinate systems, including distinctly different systems such as genetic and cytological maps.
- A gene produces a Gene PRODUCT (enzyme or other protein or subunit, or RNA), which may be further described in terms of IUB#, metabolic process, role, metabolic constituent, and pathway.
- A MUTATION in a gene produces PHENOTYPIC TRAITS.
- STOCKS carry MUTATIONS and KARYOTYPIC VARIATIONS, have ancestors, and are available from sources.
- All of the above objects in the database can be linked with REFERENCES and source PERSONS.
- Uncertainties and changes in information and measurements are accommodated.

Query Mode

The interface to the Maize DB is form-based. A query is formulated by placing the desired characteristic (e.g., phenotypic trait, mutation type, combination of specific mutants, or endpoint coordinates) into the appropriate field on the form for the object that the user wishes to retrieve. For example, to retrieve a strain with a mutation in each of the two orange pericarp genes *orp1* and *orp2*, the user enters query mode on the Strain Form and places *orp1* and *orp2* in the Mutation list field.

To obtain a list of all genes between genetic coordinates 0 and 40 on Chromosome 1, the user enters query mode on Sites and enters 20 +/- 20 in the Coordinate fields and Gene in the Type field. A Menu button converts the user's specification into the corresponding Sybase query and returns a list of all objects (stocks in the first example, genes in the second) that satisfy those constraints. Menu options then allow the user to examine selected strains or genes in detail and to draw a map of the genes.

Rapid Travel

The interface also provides for rapid travel between forms to get detailed information about components of the description. For example, in examining a strain, the user may wish to see all information and references relating to one of the mutations. Pointing to that field and pushing a menu button presents the Mutation form for that mutation entry. The user can then either return to the original form or further expand the query by pointing to the "Gene field" to find its location on the chromosome and perhaps be surprised to learn that the gene with this well-defined morphological trait, in fact, codes for a subunit of the amino acid biosynthetic gene tryptophan synthetase.

Another user may have started a query by asking for a strain with a mutation affecting tryptophan biosynthesis, and a third by specifying and selecting from all mutations affecting pericarp color. They may end up with the same set of information, and may even ultimately choose the same stock, but approach it from different perspectives and travel different routes through the database. In this manner, a wide variety of information at many levels of genetic analysis is available through paths determined by the user.

Comprehensive data entry continues; modifications and extension of the software are underway. This phase of development will emphasize extensions in the analysis and storage of both classical and RFLP mapping data. ◆

From the Hill

Plant Variety Protection: An Alternative to Patents

Janice M. Strachan, Plant Variety Examiner
Plant Variety Protection Office
USDA, Agricultural Marketing Service
Beltsville, MD

Development of a new plant cultivar or variety, either by "traditional" breeding methods or by "modern" molecular modification, requires a lot of time and effort. To recover the costs of this research and development, the breeder may seek to obtain exclusive marketing rights for the new variety. Keeping it a trade secret is one way to do this, as well as obtaining either a plant patent, utility patent, or plant variety protection. The method chosen depends on the specific benefits and limitations of the protection, and the costs involved. Plant variety protection is a good choice for many breeders.

History

The 1930 Plant Patent Act first allowed for patenting of asexually reproduced cultivars (except tubers). By the 1960s, some European countries enacted plant breeders' rights laws. It was demonstrated that sexually reproduced varieties were uniform and stable enough to be included in these laws. During the 1960s several attempts were made to enact similar protection in the United States, including a proposal to revise the Plant Patent Act to include sexually reproduced plants. These early attempts were unsuccessful.

The Plant Variety Protection (PVP) Act was enacted on December 24, 1970. Its purpose is to "encourage the development of novel varieties of sexually reproduced plants" by providing their owners with exclusive marketing rights of them in the United States. The requirements of protection are that the variety be uniform, stable, and distinct from all other varieties. Fungi, bacteria, and first generation hybrids are excluded from PVP protection. Varieties sold or used in the United States for longer than 1 year or more than 4 years in a foreign country are also ineligible for protection.

A Certificate of Protection remains in effect for 18 years from the date of issuance. The owner may specify that the variety be sold by variety name only as a class of certified seed, as defined in the Federal Seed Act. Once so specified, the designation cannot be reversed. There are two exemptions to the rights granted. One exists to allow farmers to save seed for use on their own farm or to sell it to their neighbors. Recent court decisions have defined who is a "farmer" and how much seed can be saved. Another exemption allows research to be conducted using the variety. This allows for the free exchange of germplasm within the research community.

PVP Office

The PVP Office is responsible for administering the PVP Act. It is organized within the Agricultural Marketing Service of the U.S. Department of Agriculture. Commissioner Kenneth Evans heads the PVP Office staff, which includes five plant variety examiners and three associate examiners. The PVP Office accepts approximately 270 applications per year. Since 1971, over 2,700 Certificates of Protection have been issued in over 100 crops. Almost 75 percent of them were issued within 24 months of filing the application.

Some certificates are no longer in effect due to being abandoned, withdrawn, or expired, but no PVP Certificate of Protection has been overturned in a court of law.

How To Apply

To request protection for a new variety, the applicant completes an application packet. The complete packet must contain the following items: exhibits A, B, C, and E, a seed sample, and a fee.

Exhibit A. The origin and breeding history of the variety are presented, including genealogy, breeding method, selection criteria, and evidence of uniformity and stability. Variants, predictable deviants from the standard variety description, must be described and their frequencies stated.

Exhibit B. The novelty statement lists specific characters in which the subject variety differs from all other varieties in the crop. Evidence for the differences is also included when the differences are not obvious.

Exhibit C. An objective description of the variety is given. The PVP Office has developed forms for use in describing varieties of many crops. They are constantly improving older forms or creating forms for new crops. Breeders and other knowledgeable persons are consulted before a draft form is finalized.

Exhibit E. The basis of the applicant's ownership is stated by describing how ownership was obtained.

Seed Sample. A voucher specimen of 2,500 viable seeds (85 percent or greater germination rate) is required when the application is filed. The sample is stored at the National Seed Storage Laboratory in Ft. Collins, CO. The applicants may be asked to replenish this sample if the germination rate or sample size fall below adequate levels during the protection period.

Fees. The filing fee ($250) and the examination fee ($1,900) are payable to the Treasurer of the United States. The PVP Office is completely funded by user fees, so fees may occasionally be raised to cover operating costs.

Additional information concerning the variety can by given in exhibit D. Information in this exhibit may include test-cross results, trial data, isozyme or other molecular test results, photographs, possible uses for the variety or its products, specific descriptive information not disclosed elsewhere in the application, or anything the applicant feels may be useful. This section may be omitted if the data is placed in another exhibit.

Examination Process

Once a complete application is filed in the PVP Office, the application is assigned to an examiner. The examiner conducts a literature search of the crop and gathers descriptive information on varieties from grow-out trials, release notices, seed catalogs, PVP applications, and other published sources. The examiner maintains the variety descriptions in computerized crop databases. Over 35,000 different varieties in more than 100 crops are currently in the system. The examiner then uses the appropriate database to determine the novelty of the application variety.

To be granted a Certificate of Protection, a variety must be novel based on its distinctness from all previously existing varieties, its uniformity, and its stability. These items are disclosed by the applicant in his application packet. The PVP Office does not perform grow-out trials, therefore, the applicant must gather and report all information that is required to complete the application. This information may include complete descriptions of similar varieties, color chart references, statistical analyses, photographs, plant specimens, or other information that the examiner needs to complete the evaluation of the application. If additional information is requested by the examiner, the applicant is given sufficient time to provide this information. Extensions of time can be requested by the applicant.

If the variety is found to be novel, then the certificate fee ($250) is requested and a Certificate of Protection is issued. A short summary of the basis of novelty is published in the quarterly Official Journal. The most effective novelty statement, both in exhibit B and in the Journal, is one in which the applicant states the most similar previously existing variety, and then lists the characters by which his or her variety differs from that "most similar" variety. If the application variety differs from the most similar variety, it follows that it must differ from all other varieties.

Current Issues

What is the minimum difference between varieties that indicates "distinctness"? This question has led

Some Recently Protected Varieties

Variety	Crop	Developer
Horizon	Field Bean	Asgrow Seed Co.
Wax 216 and Bush Romano 350	Garden Bean	Rogers NK Seed Co.
Primo	Garden Bean	Ferry-Morse Seed Co.
Limousine	Kentucky Bluegrass	Deutsche Saatveredelung Lippstadt
LH191, LH197, and LH 215	Corn	Holden's Foundation Seeds, Inc.
Lp215D	Corn	Wilson Seeds, Inc
PHJ90, PHK93, PHM81, PHN66, PHR03, PHR55, PHR58, and PHW30	Corn	Pioneer Hi-Bred International, Inc.
MBSJ, MBUB, MM402A, 3IBZ2, LIBC4, and 83IBI3	Corn	DeKalb Plant Genetics
Gemini	Lettuce	Sakata Seed America, Inc.
Bautista	Lettuce	Royal Sluis
XP5034	Tomato	Asgrow Seed Co.
W2501 and W2502	Wheat	AgriPro Biosciences

to many discussions within the PVP Office, its advisory board, and the breeding community at large. The PVP Act states that a novel variety is distinct when it "clearly differs by one or more identifiable morphological, physiological, or other characteristics ... from all prior varieties of public knowledge." The meanings of "characteristic" and "identifiable" are purposefully vague in this definition to allow for future advances in knowledge and methodology.

Characteristics used to describe the novelty of a variety should be stable and observable throughout the 18-year protection period. For this reason, small differences in quantifiable characteristics are seldom useful in distinguishing between varieties, no matter how statistically significant. The "importance" or "value" of characteristics to the productivity of the crop are not considered when making novelty decisions. Therefore, "cosmetic" traits, those which do not contribute to the productivity of the crop, can be used to distinguish among varieties. Some breeders argue that basing judgments on cosmetic traits trivializes a PVP certificate.

As new methods of varietal identification become available, the PVP Office consults with the plant breeding community and research experts to best use these procedures. The advent of isozyme analysis, RFLP's, RAPD's, VNTR's, and Short Tandem Repeat Length Polymorphisms has raised many questions. Should differences in nonsense regions or non-coding regions of chromosomes be allowed? If procedures for some analyses are not standardized, will database comparisons be meaningful? Who should be responsible for developing standard methods? What is a characteristic: a gene, an enzyme, a band, a base pair, or another level of information? When such information is used to establish novelty, will it remain repeatable and stable during the protection period?

As a member of the International Union for the Protection of New Varieties of Plants (UPOV), the United States provides plant variety protection to its citizens similar to what is being offered to citizens of other UPOV member countries. Recent changes in the UPOV Convention may require changes to the PVP Act to incorporate some new ideas. For example, the 1991 UPOV Convention introduces the idea of "essentially derived" varieties. The PVP

Cont. on page 22 ➤

Other Pursuits

Japan's Rice Genome Program

Susan McCarthy, Coordinator
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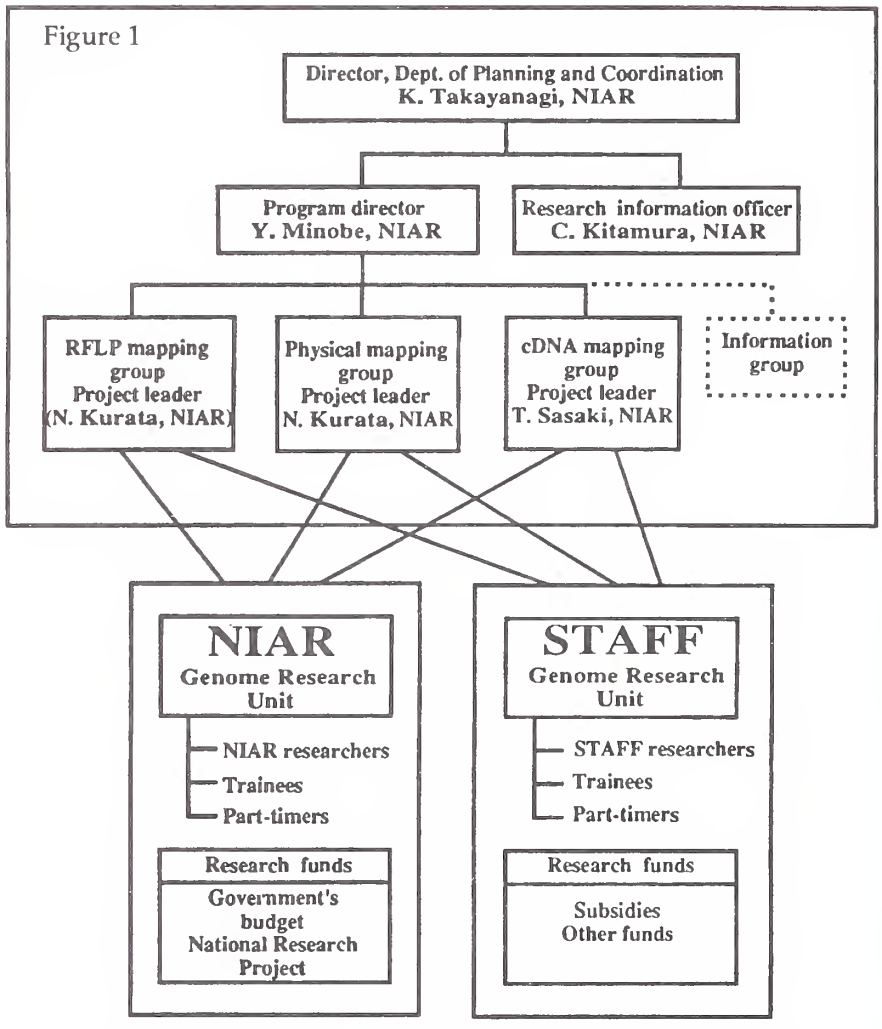
National Agricultural Library, USDA
Beltsville, MD

Japan's Rice Genome Program, initiated late last year, brings together a uniquely Japanese blend of business and government. Overall program management falls under the government's Ministry of Agriculture, Forestry, and Fisheries (MAFF). Technical direction and support come from the National Institute of Agrobiological Resources (NIAR) and the Society for Techno-innovation of Agriculture, Forestry, and Fisheries (STAFF).

NIAR is a national research institute under MAFF with research funding for genetic resources, molecular and cell biology, applied physiology, and radiation breeding. STAFF is a cooperative embracing over 130 businesses and 47 prefectures (state governments). Figure 1 depicts the program's organizational structure.

By January 1992, 40 scientists had been assigned to the Rice Genome Program. The first 7-year stage was launched October 1, 1991. Combined NIAR/STAFF program funding amounted to nearly $15 million for 1991. This year STAFF plans to begin construction of a

Figure 1



Organization of the NIAR/STAFF Rice Genome Research Program

research center in Tsukuba. The center should be completed by 1993.

Goals

Specific research goals for the program are listed below. The timetable for the program is given in figure 2.

Mapping

- Develop a physical map with DNA clones from YAC, cosmid, and phage libraries.
- Construct cDNA catalogs from several different organs, especially important for agronomic traits.
- Integrate physical and genetic maps for isolating agronomic, environmental, and economical traits.
- Accumulate detailed analyses of Chromosome-6, which carries many genes controlling disease and insect resistance, and photosensitivity.
- Research genome organization, structure, and function; leading to an understanding of allelic relationships associated with hybrid vigor, programmed differentiation, and other genetic events.

Technology Development

- Develop tools and techniques to efficiently construct individual chromosome libraries.
- Prepare easy PCR-methods to analyze segregation data on F2 populations.

Informatics

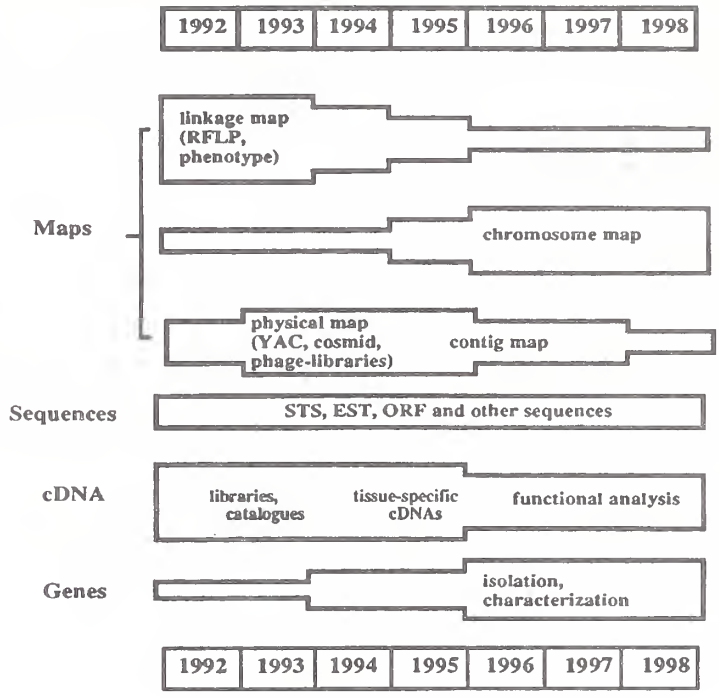
Data storage and management will be performed at NIAR as a center of DNA Bank. Included in the collection will be the chromosome maps, position assigned-clones, RFLP probes, and STS and ETS sequences. Clones and materials registered in the data bank will be available for world wide distribution.

The RFLP mapping is contracted out to STAFF. By 1995, the Japanese anticipate that 2,000 markers and conventional genes will be mapped, covering 90 percent of the genome. Some of these markers will be used in chromosomal mapping, with Chromosome-6 to be the first so analyzed.

Advisory Committee

An advisory committee, formed in March 1990, provides guidance for the program. The 13-member committee developed the objectives and research goals for the program at its inception. Heading the committee is Dr. Itaru Watanabe, Professor emeritus, School of Medicine, Keio University. A committee summary report was issued in August 1990.

Figure 2



Timetable of the NIAR/STAFF Rice Genome Research Program.

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Consult page 27 for detailed information on the Rice Genome Newsletter

Announcing

Plant Genome I

November 9-11, 1992
Town & Country Hotel, San Diego, CA

Topics

Purpose, Management, and Organization
Mapping Projects
Informatics
Beyond the Map
Forest Tree Genome Mapping
Map Generation and Analytical Mapping Software Workshop

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Particle Gun Transformation of Crop Plants -Using Electric Discharge (ACCELL™ Technology)

Paul Christou, Ph.D, Senior Scientist, and Dennis McCabe, Ph.D., Senior Scientist and Research Fellow, Agracetus Inc., Middleton, WI

The ability to deliver foreign DNA directly into regenerable cells, tissues, or organs appears to provide the best method, at present, to achieve truly genotype-independent transformation in many agronomic crops, bypassing *Agrobacterium* host-specificity and tissue culture-related regeneration difficulties. Microprojectile bombardment employs high-velocity metal particles to deliver biologically active DNA into plant cells. This concept has been described in detail by Sanford (1988). Following the original observation by Klein et al. (1987) that tungsten particles could be used to introduce macromolecules into epidermal cells of onion with subsequent transient expression of enzymes encoded by these compounds, Christou and McCabe (Christou et al., 1988) demonstrated that this process could be used to deliver biologically active DNA into living cells and produce stable transformants.

Combining the relative ease of DNA introduction into plant cells with an efficient regeneration protocol, which does not require protoplast or suspension cultures, particle bombardment is the optimum system for transformation. Important advancements and refinements using soybean (McCabe et al., 1988; Christou et al., 1990), corn (Gordon-Kamm et al., 1990; Fromm et al., 1990), and rice (Christou et al., 1991) as model systems for dicots and monocots demonstrated the power and versatility of the technique.

Developments

Methods Used

Different methods have been used to accelerate particles into living cells (Sanford et al., 1987). These include pneumatic devices; instruments utilizing a mechanical impulse or macroprojectile; centripetal, magnetic or electrostatic forces; spray or vaccination guns; and apparatus based on acceleration by shock wave, such as electric discharge. Metal particles may be coated with DNA or RNA, or they may be used to carry the genetic material into a cell from a solution of DNA or RNA surrounding the cell.

Several variables have been identified and need to be carefully considered in experiments involving transformation utilizing particle bombardment. **Physical** parameters include (1) the nature, chemical, and physical properties of the metal particles; (2) the nature, preparation, and binding of DNA onto the particles; and (3) the characteristics of the target tissue.

Environmental variables include such parameters as temperature, photoperiod and humidity of donor plants, explants, and bombarded tissues.

Biological factors include choice and nature of explant, pre-and post-bombardment culture conditions, and interactions between the introduced DNA and cytoplasmic or nuclear components.

ACCELL™ Technology

To address the majority of the variables identified as critical to the transformation process, the ACCELL™ gene delivery method was developed to permit maximum flexibility for tuning, targeting, and cell penetration. By varying the intensity of an electric discharge through a water droplet (thus creating a shock wave accelerating the DNA-coated gold particles), penetration of the target tissue can be controlled very accurately. Using this mechanism, the majority of the particles carrying the DNA can be directed to a specific cell layer. This capability is extremely important as even identical explants from different genotypes of the same species may require different acceleration conditions for optimum particle penetration.

The versatility and usefulness of particle bombardment is illustrated by the development of a genotype-independent transformation protocol for soybean (McCabe et al., 1988; Christou et al., 1990). Starting with isolated immature embryonic axes, a simple protocol permitting recovery of transgenic plants from elite varieties was developed. Based on the number of bombarded explants, the overall transformation frequency can be as high as 15 percent with germline transformation frequencies approximating 0.25 percent. Both chimeric and clonal plants can give rise to transformed progeny, with the majority of transgenic families segregating in a Mendelian fashion in the R1 and R2 generations (Christou et al., 1990).

Hundreds of independently derived soybean plants transformed by this method have maintained the foreign genes for many generations. Elite soybean varieties expressing resistance to the herbicides Basta and Roundup, engineered through particle bombardment using electric discharge, are currently undergoing large-scale field evaluation. In a parallel series of experiments, similar approaches resulted in the development of variety-independent transformation protocols for cotton (McCabe and Martinell, 1991).

Examples of transgenic crop plants expressing herbicide resistance. a. Soybean (Bialaphos); b. Cotton (Bialaphos); c. phaseolus (Bialaphos); d. soybean field trial for resistance to the herbicides Glyphosate and Bialaphos; and e. rice (Bialaphos).

Transgenic Rice Plants

Until recently, recovery of transgenic rice plants was possible only by using direct DNA transfer methods such as electroporation (e.g., Toriyama et al., 1988) or PEG-mediated transformation (e.g., Datta et al., 1990) of protoplasts. Although genetic engineering of rice had been reported, very few cultivars could be transformed using protoplast-dependent methods. ACCELL™ technology was successfully used to transform immature rice embryos (Christou et al., 1991). Transgenic plants expressing marker genes in addition to antibiotic-, herbicide-, and insect-resistance genes were obtained at frequencies >2 percent. When progeny from transgenic rice plants carrying the bar gene were sprayed with the herbicide Basta, they were shown to express total resistance to the herbicide at levels of 2000 ppm, whereas non-transgenic plants were effectively killed at levels of 250-500 ppm.

Particle bombardment is certainly not a panacea; major technical and scientific barriers need to be overcome to bring the technol-

ogy to its full potential. It is clear, however, that utilization of this technology opens the way for effective gene transfer into tissues and species that are otherwise inaccessible to genetic modifications using recombinant DNA techniques. Genetic engineering of such recalcitrant crops as those mentioned above is now possible and in some cases routine. Soybean and cotton plants that are highly resistant to commercial herbicides and insect pests will be some of the first agricultural commercial products of recombinant DNA technology. These plants are expected to be on the market well before the end of the decade (Cutler, 1991).

Additional Applications

In addition to the transformation of recalcitrant agronomic crops, woody species have been engineered using this technology. These include poplar (McCown et al., 1991), cranberry (Serres et al., 1991), and spruce (Ellis et al., 1991). A number of additional applications of particle bombardment have been recognized and are currently in use. These include transient expression studies, mechanical viral infections, gene deletion and promoter analyses, organelle and microorganism transformations, studies of basic plant development, introduction of multiple genes into plants, RNA delivery, studies of biosynthetic pathways in plants, and mammalian cell and organ transformations.

References

Christou, P., McCabe, D.E., and Swain, W.F. 1988. Stable transformation of soybean callus by DNA-coated gold particles. Plant Physiology 87:671-674.

Christou, P., McCabe, D.E., Martinell B.J., and Swain, W.F. 1990. Soybean genetic engineering--Commercial production of transgenic plants. Trends in Biotechnology 8:145-151.

Christou, P., Ford, T., and Kofron, M. 1991. Production of transgenic rice (*Oryza sativa* L.) plants from agronomically important indica and japonica varieties via electric discharge particle acceleration of exogenous DNA into immature zygotic embryos. Bio/Technology 9: 957-962.

Cutler, K. 1991. Asgrow's genetically engineered soybean has farmers excited. AgBiotechnology News 8:12.

Datta, S.K., Peterhans, A., Datta, K., and Potrykus, I. 1990. Genetically engineered fertile Indica-rice recovered from protoplasts. Bio/Technology 8:736-740.

Ellis, D., McCabe, D.E., McInnis, S., Martinell, B., Roberts, D., and McCown, B. 1991. Transformation of white spruce by electrical discharge particle acceleration. III International Congress of Plant Molecular Biology, Tucson, Arizona.

Fromm, M.E., Morrish, F., Armstrong, C., Williams, R., Thomas, J., and Klein, T.M. 1990. Inheritance and expression of chimeric genes in the progeny of transgenic maize plants. Bio/Technology 8:833-844.

Gordon-Kamm, W.J., Spencer, T.M., Mangano, M.L., Adams, T.R., Daines, R.J., Start, W.G., O'Brien, J.V., Chambers, S.A., Adams, W.R., Willetts, N.G., Rice, T.B., Mackey, C.J., Krueger, R.W., Kausch, A.P., and Lemaux, P.G. 1990. Transformation of maize cells and regeneration of fertile transgenic plants. The Plant Cell 2:603-618.

Klein, T.M., Wolf, E.D., Wu, R., and Sanford, J.C. 1987. High velocity microprojectiles for delivering nucleic acids into living cells. Nature 327:70-73.

McCabe, D.E., Swain, W.F., Martinell, B.J., and Christou, P. 1988. Stable transformation of soybean (*Glycine max*) by particle acceleration. Bio/Technology 6:923-926.

McCabe, D.E. and B.J. Martinell. 1991. Particle gun transformation applied to cotton. III International Congress of Plant Molecular Biology, Tucson, Arizona.

McCown, B.H., McCabe, D.E. Russell, D.R., Robinson, D.J., Barton, K.A., and Raffa, K.F. 1991. Stable transformation of Populus and incorporation of pest resistance by electric discharge particle acceleration. Plant Cell Reports 9:590-594.

Sanford, J.C., Klein, T.M., Wolf, E.D., and Allen, N. 1987. Delivery of substances into cells and tissues using a particle bombardment process. Journal of Particulate Science and Technology 6: 559-563.

Sanford, J.C., 1988. The Biolistic Process. Trends in Biotechnology 6:299-302.

Serres, R., Stang, E., McCabe, D., Russell, D., Mahr, D., and McCown, B. 1992. Gene transfer using electric discharge particle bombardment and recovery of transformed cranberry plants. Journal of the American Society for Horticultural Science 117:174-180.

Toriyama, K., Arimoto, Y., Uchimiya, H., and Hinata, K. 1988. Transgenic rice plants after direct gene transfer into protoplasts. Bio/Technology 6:1072-1074.

Umbeck, P., Johnson, G., Barton, K.A., and Swain, W.F. 1987. Genetically transformed cotton (*Gossypium hirsutum* L.) plants. Bio/Technology 5:263-266. ◆

Off the Wire

Using ASN.1 (Abstract Syntax Notation 1): A Data Description Language*

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Abstract Syntax Notation 1 (ASN.1) is used to describe the structure of data to be transferred between the Application Layer and the Presentation Layer of the Open Systems Interconnection (OSI) (next generation networking protocol).

ASN.1 is meant to provide a mechanism whereby the Presentation Layer can use a single standard encoding to reliably exchange any arbitrary data structure with other computer systems, while the Application Layer can map the standard encoding into any type of representation or language that is appropriate for the end user. ASN.1 does not describe the content, meaning, or structure of the data, only the way in which it is specified and encoded.

These properties make it an excellent choice for a standard way of encoding scientific data. Since ASN.1 does not specify content, specifications can be created as new concepts need to be represented. As it is an International Standards Organization (ISO) standard, the new specification can take advantage of various tools built to work with ASN.1 in general. It removes from scientists the role of specifying *ad hoc* file formats, and focuses them instead on specifying the content and structure of data necessary to convey scientific meaning.

Data Specification

There are two aspects to ASN.1--the specification of the data and the encoded data itself. The specification describes the abstract structure of the data and the allowed values various fields may take. Frequently scientific data is presented with no formal specification. There may be some documentation describing the data file, but very often it is incomplete or not entirely accurate, since it is usually written about the file rather than as a integral step toward building the file.

The ASN.1 specification is formal language, which means it can be automatically and thoroughly checked for errors and inconsistencies in form by machine before any data is collected.

Further, it can be used by a computer to validate that any data presented correctly reflects that specification. This is essential in eliminating the random errors and oversights in generating data files that plague scientific data now.

A utility program, AsnTool, was built at NCBI with the AsnTool libraries to do this sort of checking and validation while developing ASN.1 specifications. (For information on obtaining AsnTool, see the end of the article.)

The requirement for a separate specification also means that interested parties can examine and evaluate the structure of the data independent of any particular database or data file. One can understand the limits and strengths of a specification separately from the quality or amount of the data itself. Data structures that prove to be useful can be re-used in a variety of ways--by large public databases, by small private databases, in various software tools, and in assorted data files.

*Note to Readers: This article briefly describes ASN.1 but it is not meant to be an explanation or tutorial on ASN.1 itself. Please see the Reference section for such works.

Finally, a separate specification means software to construct, decode, and validate any ASN.1 specified object can be built fully or semi-automatically from the specification. Data encoded according to that specification can then be processed with relatively little manual programming for those aspects of the application dealing directly with ASN.1. This is the purpose of the AsnTool routines.

Commercial Tools

A number of commercial and public domain tools are available for working with ASN.1 and for automatically building data handlers of various sorts. They are focused on the use for which ASN.1 was originally intended, the exchange of data between layers of the OSI. As such they tend to automate the process more that AsnTool does, because the domain of use is more limited. The fact that they determine the internal data structures to use and write all the code to handle them themselves is not a big problem in this case.

When ASN.1 is used for scientific data description, however, other uses will be made of the encoded data than may have originally been envisaged by the designers of these products. For example, a scientist will often want an application which scans through a large complicated data structure and extracts certain fields for use, or even just counts occurrences of certain values. A tool that automatically generates large elaborate data structures and lots of code to parse the stream, generate the structures, and store them in memory is inappropriate for such an application. Further, a scientific application may well wish to manipulate that data in a different language than the tool is written in, such as FORTRAN, PROLOG, or LISP. These applications may well wish to store the whole data structure from the stream, but they will not wish to use the data structure provided by the tool.

Encoding

ASN.1 can be used to encode data in two ways, an ASCII human readable form called "value notation" or "print form," a binary encoding. ASN.1 has separate standards documents for the syntax (specification rules) and the binary encoding rules (BER, or "Basic Encoding Rules"). This was done on purpose to allow various encoding rules for the same abstract syntax. The BER is, at this writing, the only official ISO encoding for ASN.1, but several other encodings, which are faster or take less space, are under consideration by ISO. Currently the only binary encoding AsnTool supports is BER.

The value notation, or ASCII form of the data, is not really an official ISO standard. It was meant to provide a human readable form of ASN.1 data for development or explication, but not as a standard for data exchange. Nonetheless, value notation is quite robust for data exchange. These rules are listed in appendix 1.

While we do not recommend the ASCII form of ASN.1 encoded data for large amounts of data, it is useful for developing and testing data representations or for easily generating ASN.1 values from other data files or local databases without specialized tools. Since the value notation and binary encoded forms of data are completely and reliably interconvertible using AsnTool, there is no problem doing this.

Ordering Information

AsnTool is available for anonymous ftp from ncbi.nlm.nih.gov as /toolbox/ncbi_tools/ncbi.tar.Z.

If you have questions or comments about AsnTool, you may send an E-mail request to asntool@ncbi.nlm.nih.gov (Internet), or write to the following address: AsnTool, National Center for Biotechnology Information, Building 38A, NIH, 8600 Rockville Pike, Bethesda, MD 20894.

References

The Open Book A Practical Perspective on OSI by Marshall T. Rose, Prentice Hall, Englewood Cliffs, NJ 07632 (c) 1990

ISO Development Environment (public software), University of Pennsylvania Department of Computer Science and Information Science

Moore School, Attn: David J. Farber (ISODE Distribution), 200 South 33rd Street, Philadelphia, PA 19104-6314

OSIkit Tools for NIST (1989) (public software), U.S. Department of Commerce, National Institute of Standards and Technology, Gaithersburg, MD

Information Processing - Open Systems Interconnection - Specification of Abstract Syntax Notation One (ASN.1). International Organization for Standardization and International Electrotechnical Committee, 1987. International Standard 8824.

Information Processing - Open Systems Interconnection - Specification of Basic Encoding Rules for Abstract Syntax Notation One (ASN.1).

International Organization for Standardization and International Electrotechnical Committee, 1987. International Standard 8825.

Information Processing - Open Systems Interconnection - Abstract Syntax Notation One (ASN.1) - Draft Addendum 1: Extensions to ASN.1. International Organization for Standardization and International Electrotechnical Committee, 1987. Draft Addendum 8824/DAD 1.

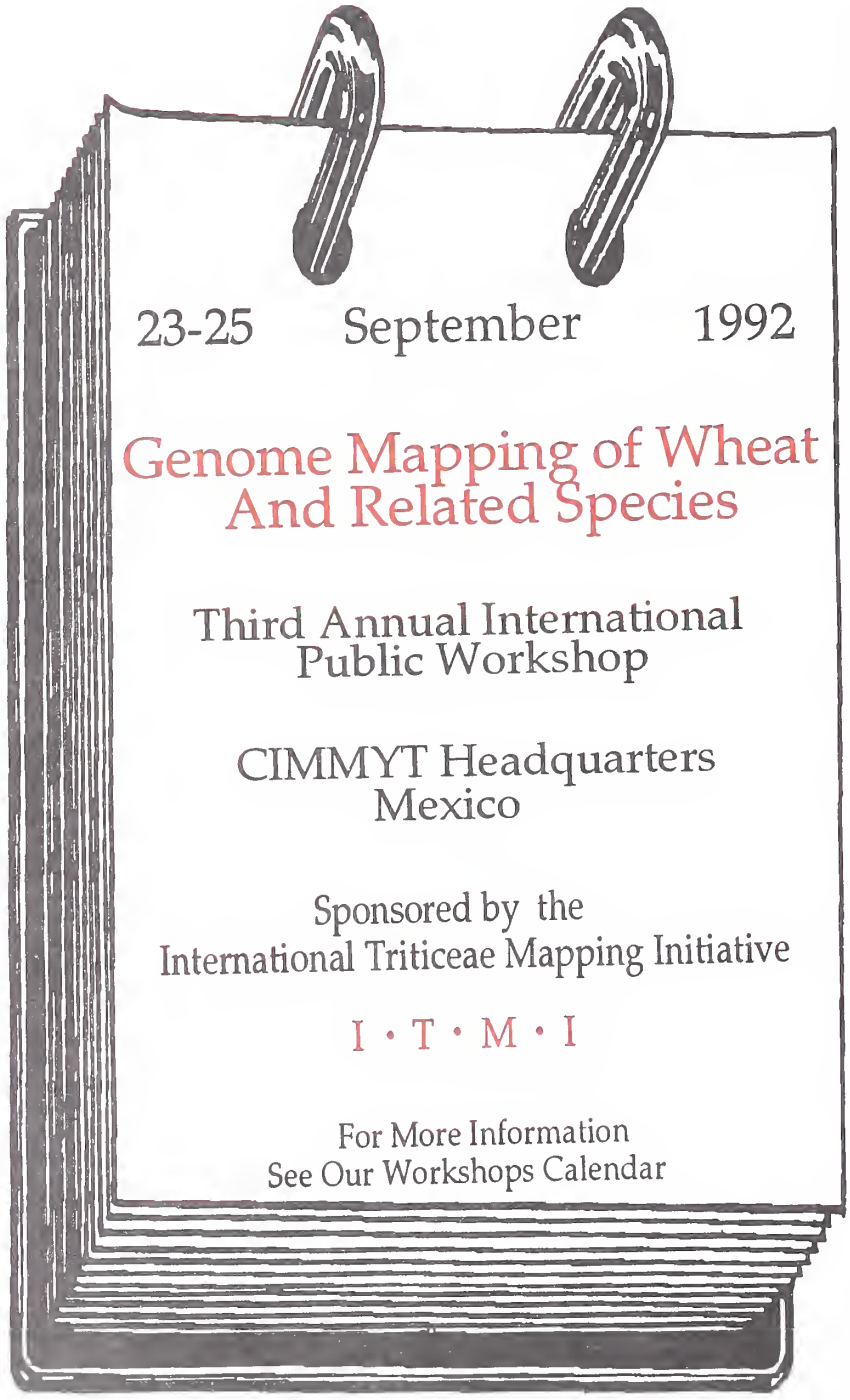
Information Processing - Open Systems Interconnection - Abstract Syntax Notation One (ASN.1) - Draft Addendum 1: Extensions to ASN.1 Basic Encoding Rules. International Organization for Standardization and International Electrotechnical Committee, 1987. Draft Addendum 8825/DAD 1. ◆

For the Plant Genome perspective on ASN.1 see Douglas Bigwood's article on page 7.

PVP--*Continued from page 13*

Office and the U.S. plant breeding community are discussing this and other issues in the UPOV Convention, and how they may affect plant variety rights if included in the PVP Act.

Plant breeding is a dynamic industry, mingling the old methods with new technology to its best advantage. The PVP Office also mingles the old and new methods when determining the novelty of a plant variety. Their effectiveness shows in the growth of the breeding industry since 1970. To apply for protection, or to get more information about the PVP Act, write to: USDA, AMS, Plant Variety Protection Office, NAL Building, Room 500, Beltsville, MD 20705-2351 (Tel: 301-504-5518). ◆



Introducing Dr. Duane Acker

Dr. Duane Acker is the new Assistant Secretary of Agriculture for Science and Education. He was sworn in June 10 by Secretary of Agriculture Edward Madigan. President George Bush nominated him to the post in March. His nomination was confirmed June 9 by the U.S. Senate.

As assistant secretary, Dr. Acker will oversee four U.S. Department of Agriculture agencies responsible for agricultural research and education involving production and use of animals and plants, development of new products, and the use and conservation of soil, water, forest, and air resources. Those agencies are USDA's Agricultural Research Service, Cooperative State Research Services, Extension Service, and the National Agricultural Library.

Prior to his appointment, Dr. Acker was administrator of USDA's Foreign Agricultural Service (FAS) and Office of International Cooperation and Development (OICD). He was appointed administrator of OICD in February of 1990 and of FAS in January of 1991.

"Duane has done a superb job as administrator of FAS and OICD" Madigan said. "With his exceptional leadership qualities and his extensive experience in agricultural research and university administration, I know he will be successful with his new responsibilities as head of Science and Education."

Before joining USDA, Dr. Acker was director and then assistant to the administrator for food and agriculture at the U.S. Agency for International Development from 1986 to January 1990.

Dr. Acker served as president of Kansas State University from 1975 to 1986. Before that he was the associate dean of agriculture for instruction at Kansas State, dean of agriculture and biological sciences and director of extension and the experiment station at South Dakota State University, and vice-chancellor for agriculture and natural resources at the University of Nebraska. Dr. Acker worked as a county extension 4-H agent during the summer of 1950. He was an animal science instructor at Oklahoma State University from 1953 to 1955 and at Iowa State University from 1955 to 1962. He also worked as a consultant to the feed industry while at Iowa State University.

Dr Acker has reviewed food and agricultural programs in more than 20 countries. He served from 1983 to 1986 as an appointee of President Ronald Reagan on the Board for International Food and Agricultural Development.

He is a member of numerous professional and honorary organizations, and has published a number of works on agriculture-related topics, including a widely used animal science textbook.

Dr. Acker has been a director of the U.S. Council on Agricultural Science and Technology, chair of the U.S. Deans of Agriculture, chair of the agriculture section of the American Association for the Advancement of Science, president of Gamma Sigma Delta, and a member of the National Academy of Sciences' Commission on Education in Agriculture and Natural Resources.

Dr. Acker is a native of Atlantic, Iowa. He received his Ph.D. in animal nutrition from Oklahoma State University, Stillwater, in 1957, a B.S. degree in animal science and a degree in animal nutrition from Iowa State University in 1952 and 1953, respectively. ◆

Calendar of Upcoming Genome Events

MEETINGS - 1992

September 23-25: **Genome Mapping of Wheat and Related Species, Third Annual International Public Workshop,** CIMMYT Headquarters, Mexico. Contact: Dr. David Hoisington, CIMMYT, Lisboa 27, Apdo. Postal 6-641, 06600 Mexico, DF Mexico. Telephone: Ms. S. Velazquez 5-25-954-2100 ext. 1382, FAX: 5-25-954-1069.

September 26-30: **Genome Sequencing and Analysis Conference IV,** Hilton Head, SC. Contact: Susan Wallace, P.O. Box 541, Rockville, MD 20848. Telephone: (301) 480-0634, FAX: (301) 480-8588.

October 14-17: **Human Genome '92: The Human Genome Project International Conference,** Nice, France. Contact: American Association for the Advancement of Science Meetings Office, 1333 H St., NW, Washington, DC 20005. Telephone: (202) 326-6461, FAX: (202) 289-4021.

November 7-11: **Program in Mathematics and Molecular Biology III: Computational Approaches to Nucleic Acid Structure and Function,** Sante Fe, NM. Contact: Dr. S.J. Spengler, Math. & Molecular Biology, 103 Donner Laboratory, University of California, Berkeley, CA 94720. FAX: (510) 642-4071.

November 8-11: **2nd International Conference on DNA Fingerprinting,** Belo Horizonte, Brazil. Contact: Prof. Sergio D.J. Pena, Nucleo de Genetica Medica de Minas Gerais, Avenida Alfonso Pena, 3111-9 Andar, Caixa Postal 3396, CEP 30112, Belo Horizonte, MG, Brazil.

November 9-11: **Plant Genome I,** San Diego, CA. Contact: Scherago International, Inc., 11 Penn Plaza, Ste 1003, New York, NY 10001. Telephone: (212) 643-1750, FAX: (212) 643-1758.

November 15-19: **The American Society for Cell Biology Thirty-Second Annual Meeting,** Denver, CO. Contact: American Society for Cell Biology Meeting Office, 9650 Rockville Pike, Bethesda, MD 20814-3992. Telephone: (301) 530-7153, FAX: (301) 530-7139.

WORKSHOPS AND COURSES - 1992

October 12-15: **PCR Techniques & DNA Sequencing Lecture Course,** Lake Tahoe, NV. Contact: Center for Advanced Training in Cell and Molecular Biology, The Catholic University of America, 620 Michigan Ave., NE, Washington, DC 20064. Telephone: (202) 319-6161, FAX: (202) 319-4467.

October 12-15: **Recombinant DNA Methodology & DNA Sequencing Lecture Course,** Lake Tahoe, NV. Contact: Center for Advanced Training in Cell and Molecular Biology, The Catholic University of America, 620 Michigan Ave., NE, Washington, DC 20064. Telephone: (202) 319-6161, FAX: (202) 319-4467.

FUTURE EVENTS

January 5-8, 1993: **Biotechnology Computing Track, Hawaii International Conference on System Science.** Kauai, HI. Contact Lawerence Hunter, National Library of Medicine, NIH, Bethesda, MD. INTERNET: hunter@work.nlm.nih.gov, Telephone: (301) 496-9300.

January 9-15, 1993: **Keystone Symposia on Molecular & Cellular Biology: The Extracellular Matrix of Plants: Molecular, Cellular and Developmental Biology,** Santa Fe, NM. Contact: Keystone Symposia, Drawer 1630, Silverthorne, CO 80498. Telephone: (303) 262-1230.

January 17-22, 1993: **Miami Bio/Technology Winter Symposia, Advances in Gene Technology: Protein Engineering and Beyond,** Miami, FL. Contact: Sandra Black, P.O. Box 016129, Miami, FL 33101. Telephone: (800) 642-4363, FAX: (305) 324-5665.

January 26-February 1, 1993: **Keystone Symposia on Molecular & Cellular Biology: Evolution and Plant Development,** Taos, NM. Contact: Keystone Symposia, Drawer 1630, Silverthorne, CO 80498. Telephone: (303) 262-1230.

February 8-14, 1993: **Keystone Symposia on Molecular & Cellular Biology: Genetic and In Vitro Analysis of Cell Compartmentalization,** Taos, NM. Contact: Keystone Symposia, Drawer 1630, Silverthorne, CO 80498. Telephone: (303) 262-1230.

February 23-March 1, 1993: **Keystone Symposia on Molecular & Cellular Biology: Nucleases: Structure, Function and Biological Roles,** Tamarron, CO. Contact: Keystone Symposia, Drawer 1630, Silverthorne, CO 80498. Telephone: (303) 262-1230.

March 7-14, 1993: **Keystone Symposia on Molecular & Cellular Biology: Frontiers of NMR in Molecular Biology-III,** Taos, NM. Contact: Keystone Symposia, Drawer 1630, Silverthorne, CO 80498. Telephone: (303) 262-1230.

March 31-April 3, 1993: **Twelfth Annual Symposium: Current Topics in Plant Biochemistry, Molecular Biology and Physiology,** Columbia, MO. Contact: Doug Randall, 117 Schweitzer Hall, University of Missouri-Columbia, Columbia, MO 65211. Telephone: (314) 882-7796, FAX: (314) 882-5635.

April 18-25, 1993: **Keystone Symposia on Molecular & Cellular Biology: Transposition and Site-Specific Recombination: Mechanism and Biology,** Keystone, CO. Contact: Keystone Symposia, Drawer 1630, Silverthorne, CO 80498. Telephone: (303) 262-1230.

April 21-25, 1993: **Molecular Genetics of Plant-Microbe Interactions (Workshop and Symposia),** East Brunswick, NJ. Contact: Rutgers, State University of New Jersey, Registration Desk, Office of Continuing Professional Education, Cook College, P.O. Box 231, New Brunswick, NJ 08903. Telephone: (908) 932-9271, FAX: (908) 932-8726.

May 8-13, 1994: **HPLC'94, Eighteenth International Symposium on High Performance Liquid Chromatography,** Minneapolis, MN. Contact: Barr Enterprises, P.O. Box 279, Walkerville, MD. Telephone: (301) 898-3772, FAX: (301) 898-5596.

June 5-9, 1993: **Congress on Cell and Tissue Culture: 1993 Meeting of the Tissue Culture Association. Growth Control: From the Receptor to the Nucleus,** San Diego, CA. Contact: Congress on Cell and Tissue Culture, 8815 Center Park Drive, Suite 210, Columbia, MD 21045. Telephone: (410) 992-0946.

June 16-21, 1996: **HPLC'96, Twentieth International Symposium on High Performance Liquid Chromatography,** San Francisco, CA. Contact: Barr Enterprises, P.O. Box 279, Walkerville, MD. Telephone: (301) 898-3772, FAX: (301) 898-5596.

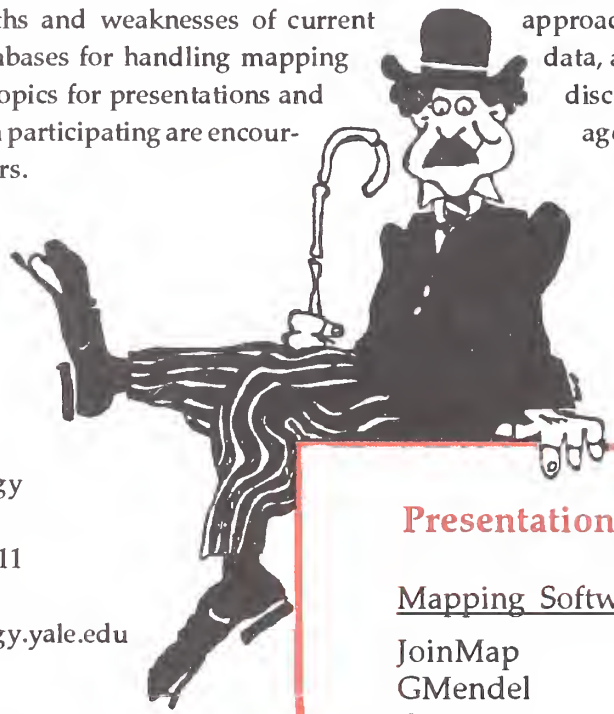
Vacancy Announcement

Molecular Geneticist/Biologist: a 2-year appointment beginning approximately 1 October 1992 to implement molecular strategies and techniques needed to describe plant genetic uniqueness and genomic variation. Various DNA technologies including single locus and multilocus PCR-based typing/fingerprinting, and related STS-based mapping strategies will be employed. Experience in molecular genetics, particularly sequencing, mapping, and informatics is essential. Send curriculum vitae and three letters of recommendation to: Dr. Stephen Kresovich, USDA-ARS, Plant Genetic Resources Unit, Cornell University, Geneva, NY 14456-0462; Tel: 315-787-2244.

ARS is an Equal Opportunity Employer.

Mapping Software Workshop-- November 8, 1992

An informal workshop preceding the International **Plant Genome I** conference is being offered. The workshop will present and demonstrate current mapping and graphical pedigree software. Software developers and research scientists will discuss the strengths and weaknesses of current approaches and future needs. Databases for handling mapping data, analysis, and maps will also be topics for presentations and discussions. Parties interested in participating are encouraged to contact one of the organizers.



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Presentations:

Mapping Software

JoinMap
GMendel
Cprop
MapMaker

Graphical Pedigree Software

HyperGene

Newsletter "Rice Genome" Launched

The Rice Genome Research Program (RGP) has produced the first issue of its newsletter, titled "Rice Genome". The newsletter aims to inform all researchers interested in mapping and analyzing plant genomes. The main objective is to enhance international cooperative research efforts for rice genome analysis and for the isolation and utilization of useful rice genes in plant breeding and biotechnology.

Funding is provided by the Ministry of Agriculture, Forestry and Fisheries (MAFF), Japan, and the Japan Racing Association (JRA).

The newsletter "Rice Genome"

The first issue of the newsletter "Rice Genome" (Number 1, vol. 1, July 1992) contains articles on the following topics:

- an overview of the Rice Genome Research Program
- the current strategy of cDNA cataloging
- RFLP linkage mapping
- physical mapping and chromosome mapping

In addition, information is given on how to request DNA clones (cDNA and RFLP landmarkers).

The newsletter is available free of charge. To have your name added to the mailing list, send your name and address to the address below. Please indicate also the source of this announcement.

Editorial Office of Rice Genome
Rice Genome Research Program (RGP)
National Institute of Agrobiological Resources
2-1-2, Kannondai
Tsukuba
Ibaraki 305
Japan
FAX: +81-298-38-7468

The next issue of the newsletter will be published in late autumn 1992. We welcome news items and articles on rice genome mapping and analysis from the international research community.

Probe

ISSN: 1057-2600

The official quarterly publication of the USDA Plant Genome Research Program. This newsletter is aimed at facilitating interaction throughout the plant genome mapping community and beyond.

Probe is a publication of the Plant Genome Data and Information Center, National Agricultural Library.

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Articles, announcements, and suggestions are welcome.

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National Agricultural Library

Plant Genome Publications

The following publications are available. If you would like to receive a copy, check off the title and mail your request to:

Plant Genome Data and Information Center
National Agricultural Library, Rm 1402
10301 Baltimore Blvd.
Beltsville, MD 20705-2351

Nucleotide Sequence Listings:

GenBank® nucleotide sequence databank was searched by species. A list was compiled giving the GenBank® locus name and a brief description of the sequence.

365 *Zea mays* Nucleic acid sequences. Susan McCarthy and Terrance Henrichs. A GenBank® search. 9 pp.

193 *Glycine max* Nucleic acid sequences. Susan McCarthy and Terrance Henrichs. A GenBank® search. 6 pp.

289 *Triticum aestivum* Nucleic acid sequences. Susan McCarthy and Terrance Henrichs. A GenBank® search. 8 pp.

243 *Arabidopsis thaliana* Nucleic acid sequences. Susan McCarthy and Terrance Henrichs. A GenBank® search. 7 pp.

Quick Bibliographies:

The AGRICOLA bibliographic database was searched by topic. A bibliography was compiled of the relevant citations; abstracts are included when available.

Plant Genome Analysis Techniques: Electroporation Methods and Applications. January 1986 - December 1991. 150 citations. 48 pp. Prepared by Deborah Y. Richardson. QB 92-34

Economic Aspects of Agricultural Bio/Technology. January 1986 - March 1992. 189 citations. In Press. Prepared by Nalini Basavaraj. QB 92-60

Plant Genome: Breeding for Cold Tolerance in Plants. January 1970 - March 1992. 212 citations. In Press. Prepared by Deborah Y. Richardson. QB 92-62

Miscellaneous Publications:

Data Resources and the Plant Genome Research Program. A report by the Plant Genome Database Subcommittee. June 1990. 75 pp.

Notes to Indexers No. 21, revised March 1992. Subject: Molecular Sequence Data. This note describes indexing changes for AGRICOLA records containing sequence data. 2 pp.

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